

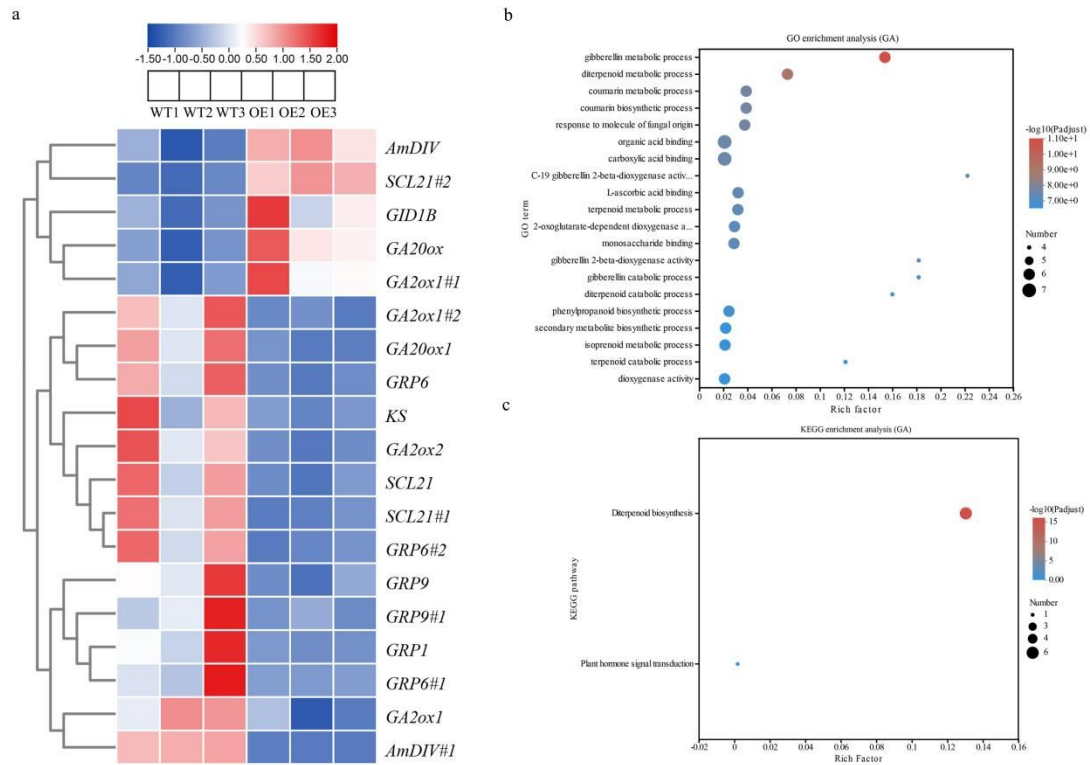


Fig. S17. Overexpression of *Flfbp1* in *F. lateritium* reshapes the gibberellin (GA) pathway transcriptome in *N. benthamiana*. *N. benthamiana* plants were inoculated with WT or *Flfbp1*^{OE} strains, and samples were collected at 10 days post-inoculation for transcriptome sequencing to analyze the expression changes of GA pathway genes. (a) Heatmap of GA pathway gene expression. (b) GO functional enrichment analysis of differentially expressed genes. (c) KEGG pathway enrichment analysis of differentially expressed genes. Genes were clustered based on their expression patterns across treatments. Color scale: blue, down-regulated; red, up-regulated. Compared with WT, infection with *Flfbp1*^{OE} resulted in the down-regulation of most genes in the GA pathway. GO and KEGG enrichment analyses revealed significant changes in functions related to hormone signal transduction and growth and development. Each treatment contained three biological replicates, and the results were consistent. KEGG (Kyoto Encyclopedia of Genes and Genomes) pathway enrichment analysis was performed to annotate the functions of differentially expressed genes, using the KEGG database (<https://www.kegg.jp/>). The enrichment significance was calculated based on the hypergeometric distribution, and pathways with $\text{Padjust} < 0.05$ were considered significantly enriched. The results were visualized as a bubble plot.